	Type	L #	Hits	Search Text	DBs
1	BRS	L1	111019	sequenc$6 near8 (rna or dna or polymer or molecule)	US-PGPUB; USPAT
2	BRS	L2	12457	tunnel$6 near8 current	US-PGPUB; USPAT
3	BRS	L3	166	l1 and l2	US-PGPUB; USPAT
4	BRS	L4	136	l3 and (nanoelectrode or electrode or contact)	US-PGPUB; USPAT
5	BRS	L5	13	l4 and signal near8 (processor or generator)	US-PGPUB; USPAT
6	BRS	L6	114	1 and nanochannel	US-PGPUB; USPAT
7	BRS	L7	124	1 and (nanochannel or nanogap)	US-PGPUB; USPAT
8	BRS	L8	17	2 and (nanochannel or nanogap)	US-PGPUB; USPAT
9	BRS	L9	16	l8 and (nanoelectrode or electrode or contact)	US-PGPUB; USPAT

	Time Stamp	Comments	Error Definition	Errors
1	2006/02/17 18:33			
2	2006/02/17 18:34			
3	2006/02/17 18:34			
4	2006/02/17 18:36			
5	2006/02/17 18:36			
6	2006/02/17 18:36			
7	2006/02/17 18:36			
8	2006/02/17 18:36			
9	2006/02/17 18:36			

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 NEWS  6  DEC 14   CA/CAplus to be enhanced with updated IPC codes
 NEWS  7  DEC 21   IPC search and display fields enhanced in CA/CAplus with the
                   IPC reform
 NEWS  8  DEC 23   New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                   USPAT2
 NEWS  9  JAN 13   IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
 NEWS 10  JAN 13   New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
                   INPADOC
 NEWS 11  JAN 17   Pre-1988 INPI data added to MARPAT
 NEWS 12  JAN 17   IPC 8 in the WPI family of databases including WPIFV
 NEWS 13  JAN 30   Saved answer limit increased
 NEWS 14  JAN 31   Monthly current-awareness alert (SDI) frequency
                   added to TULSA

 NEWS EXPRESS  FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
               CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
               V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT
               http://download.cas.org/express/v8.0-Discover/

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```
=> s sequenc? (s) (rna or dna or polymer or molecule)
         832144 SEQUENC?
         302329 RNA
          24580 RNAS
         306815 RNA
                   (RNA OR RNAS)
         756713 DNA
          18301 DNAS
         759566 DNA
                   (DNA OR DNAS)
        1048614 POLYMER
         860052 POLYMERS
        1417289 POLYMER
                   (POLYMER OR POLYMERS)
          49758 MOLECULE
         151328 MOLECULES
         194221 MOLECULE
                   (MOLECULE OR MOLECULES)
        2318132 MOL
         623046 MOLS
        2656690 MOL
                   (MOL OR MOLS)
        2694822 MOLECULE
                   (MOLECULE OR MOL)
L1       310937 SEQUENC? (S) (RNA OR DNA OR POLYMER OR MOLECULE)

=> s tunnel? (s) current
         101949 TUNNEL?
         764900 CURRENT
          99384 CURRENTS
         808283 CURRENT
                   (CURRENT OR CURRENTS)
L2        13495 TUNNEL? (S) CURRENT

=> s l1 and l2
L3           11 L1 AND L2

=> s (nanoelectrode or nanogap or nanochannel or contact or electrode)
            216 NANOELECTRODE
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            296 NANOELECTRODES
            367 NANOELECTRODE
                  (NANOELECTRODE OR NANOELECTRODES)
             98 NANOGAP
             43 NANOGAPS
            118 NANOGAP
                  (NANOGAP OR NANOGAPS)
            347 NANOCHANNEL
            461 NANOCHANNELS
            654 NANOCHANNEL
                  (NANOCHANNEL OR NANOCHANNELS)
         460924 CONTACT
         112598 CONTACTS
         519450 CONTACT
                  (CONTACT OR CONTACTS)
         456284 ELECTRODE
         340465 ELECTRODES
         588575 ELECTRODE
                  (ELECTRODE OR ELECTRODES)
L4      1058484 (NANOELECTRODE OR NANOGAP OR NANOCHANNEL OR CONTACT OR ELECTRODE
                )

=> s l3 and l4
L5            7 L3 AND L4

=> s optical (s) tweezer?
         864860 OPTICAL
             19 OPTICALS
         864868 OPTICAL
                  (OPTICAL OR OPTICALS)
           1641 TWEEZER?
L6          810 OPTICAL (S) TWEEZER?

=> s l5 and l6
L7            0 L5 AND L6

=> s l2 and l6
L8            0 L2 AND L6

=> s l1 and l6
L9           25 L1 AND L6

=> display l3 1-11 ibib abs

L3   ANSWER 1 OF 11  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2006:76824  CAPLUS
DOCUMENT NUMBER:          144:145999
TITLE:                    Determining the identity of a monomeric residue of a
                          biopolymer by resonance tunneling and fluorescence
                          quenching
INVENTOR(S):              Joyce, Timothy H.
PATENT ASSIGNEE(S):       USA
SOURCE:                   U.S. Pat. Appl. Publ., 25 pp.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.         DATE
     ---------------      ----   --------    --------------------    --------
     US 2006019259         A1    20060126    US 2004-898586          20040722
PRIORITY APPLN. INFO.:                       US 2004-898586          20040722
AB   The present invention provides a method and apparatus for determining the
identity of
```

a monomeric residue of a biopolymer. The apparatus comprises a substrate having a nanopore, a potential-producing element for producing a ramped potential across electrodes adjacent to the nanopore, and a quenchable excitable moiety adjacent to the nanopore. As a biopolymer passes through the nanopore, the identity of monomeric residues of a biopolymer may be determined by detecting changes in (a) current across the electrodes and (b) a signal of the quenchable excitable mol. The subject method and apparatus find use in determining the identity of a plurality of monomeric residues of a biopolymer, and, as such, may be employed in a variety of diagnostic and research applications.

L3 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1000661 CAPLUS
DOCUMENT NUMBER: 143:263022
TITLE: Biomol. structure determination method and device
INVENTOR(S): Tomita, Tsukasa
PATENT ASSIGNEE(S): Shimazu Corporation, Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 6 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2005245369	A2	20050915	JP 2004-63310	20040308
PRIORITY APPLN. INFO.:			JP 2004-63310	20040308

AB A method and a device for determining of nucleic acid and protein sequences are offered. MRNA precursor is synthesized with **DNA sequence** as a template and with **RNA** polymerase as catalyst which is immobilized on a base plate and taking **DNA** onto the plate or sending **DNA** out off the plate. A probe of scanning **tunnel** microscope is set on the side of the position where DNA is possible to be taken into RNA polymerase by using piezo scanner and piezo scanner driving circuit and the distance from DNA to the probe is kept so that the **tunnel current** is possible to be measured. The **tunnel current** which flows between DNA and STM probe is measured by the **tunnel current** circuit and the DNA bases are identified from the forms of the **tunnel** spectrum.

L3 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1000605 CAPLUS
DOCUMENT NUMBER: 143:261369
TITLE: Method and apparatus for nucleic acid sequencing through tunneling conductance variation detection
INVENTOR(S): Zhu, Miao
PATENT ASSIGNEE(S): Agilent Technologies Inc., USA
SOURCE: Eur. Pat. Appl., 14 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1574837	A1	20050914	EP 2004-25332	20041025
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
US 2005202444	A1	20050915	US 2004-797651	20040310
JP 2005257687	A2	20050922	JP 2005-67538	20050310
PRIORITY APPLN. INFO.:			US 2004-797651 A	20040310

AB Method and apparatus for nucleic acid sequencing through tunneling conductance variation detection are disclosed. The method involves centering a bias voltage across a pair of nanoelectrode,s separated by a channel, that corresponds to one of any of the energy differences between any two internal energy levels of a mol. of interest, and modulating the bias voltage with a modulation waveform while the mol. of interest is in the channel. An elec. signal characteristic of the mol. of interest is derived from the **tunneling current** between the nanoelectrodes, and the characteristic elec. signal is compared with known values of the signal for chemical-known mols. in order to identify the mol. of interest. Multiple pairs of nanoelectrodes may be employed to identify more reliably a single mol. or multiple mols.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:702959 CAPLUS

DOCUMENT NUMBER: 142:50803

TITLE: Electronic transport and thermopower in aperiodic **DNA sequences**

AUTHOR(S): Roche, Stephan; Macia, Enrique

CORPORATE SOURCE: Commissariat a l'Energie Atomique, DSM/DRFMC/SPSMS, Grenoble, 38054, Fr.

SOURCE: Modern Physics Letters B (2004), 18(17), 847-871
CODEN: MPLBET; ISSN: 0217-9849

PUBLISHER: World Scientific Publishing Co. Pte. Ltd.

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review. A detailed study of charge transport properties of synthetic and genomic **DNA sequences** is reported. Genomic sequences of the chromosome 22, λ-bacteriophage, and D1s80 genes of Human and Pygmy chimpanzee are considered in this work, and compared with both periodic and quasiperiodic (Fibonacci) sequences of nucleotides. Charge transfer efficiency is compared for all these different sequences, and large variations in charge transfer efficiency, stemming from sequence-dependent effects, are reported. In addition, basic characteristics of **tunneling currents**, including contact effects, are described. Finally, the thermoelec. power of nucleobases connected in between metallic contacts at different temps. is presented.

REFERENCE COUNT: 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:410279 CAPLUS

DOCUMENT NUMBER: 141:256022

TITLE: Interchain versus intrachain hole transmission through desoxyribonucleic acid molecular wires

AUTHOR(S): Bittner, Eric R.

CORPORATE SOURCE: Dep. Chem. Cent. Mater. Chem., Univ. Houston, Houston, TX, 77204, USA

SOURCE: Los Alamos National Laboratory, Preprint Archive, Condensed Matter (2004) 1-7, arXiv:cond-mat/0405228, 11 May 2004
CODEN: LNCMFR
URL: http://xxx.lanl.gov/pdf/cond-mat/0405228

PUBLISHER: Los Alamos National Laboratory

DOCUMENT TYPE: Preprint

LANGUAGE: English

AB We present a methodol. for computing the current-voltage response of a mol. wire within the Landauer-Buttiker formalism based upon transforming the cumulative transmission probability into an eigenvalue problem. The method is extremely simple to apply since does not involve construction of the mol. Greens function, and hence avoids the use of complex integration contours to avoid poles. We use this method to study the effect of

base-pair **sequence** on the conductivity of holes in **DNA** chains containing A-T bridges between guanine chains. Our results indicate that sequence plays a substantial role in ballistic transport via tunneling resonances tuned by sequence and interchain interactions. We also find that ballistic transport is dominated by intrachain transport and that hole transmission is insensitive to interchain fluctuations.

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:796982 CAPLUS
DOCUMENT NUMBER: 139:272035
TITLE: Methods and probes for nucleic acid sequencing using single electron molecular orbital tunneling spectroscopy
INVENTOR(S): Brousseau, Louis C., III
PATENT ASSIGNEE(S): Quantum Logic Devices, Inc., USA
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003083437	A2	20031009	WO 2003-US8813	20030321
WO 2003083437	A3	20031218		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-366840P P 20020322

AB A nano-probe for performing single electron MO tunneling spectroscopy (SEMOTS) is disclosed. Unlike the conventional probes, the nano-probe is capable of obtaining highly resolved spectra of single mol. electronic structures on conductive surfaces. The increase in spectral resolution allows the unique spectrum of adsorbed mols. to be collected into a database and subsequently used to identify adsorbates on surface on unknown samples. The nano-probe can be utilized for genetic **sequencing** of single **mols**. of deoxyribose nucleic acid and other oligonucleotides based on the differences in orbital energy spectra of the nucleotide bases.

L3 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:590447 CAPLUS
DOCUMENT NUMBER: 139:129083
TITLE: **DNA** and **RNA sequencing** by nanoscale reading through programmable electrophoresis and nanoelectrode-gated tunneling and dielectric detection
INVENTOR(S): Lee, James W.; Thundat, Thomas G.; Greenbaum, Elias
PATENT ASSIGNEE(S): UT-Battelle, LLC, USA
SOURCE: U.S. Pat. Appl. Publ., 24 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003141189	A1	20030731	US 2002-55881	20020128
US 6905586	B2	20050614		
PRIORITY APPLN. INFO.:			US 2002-55881	20020128

AB An apparatus and method is provided for performing nucleic acid (**DNA** and/or **RNA**) **sequencing** on a single **mol**. The genetic **sequence** information is obtained by probing through a **DNA** or **RNA mol**. base-by-base at nanometer scale as though looking through a strip of movie film. This **DNA sequencing** nanotechnol. has the theor. capability of performing **DNA sequencing** at a maximal rate of about 1,000,000 bases per s. This enhanced performance is made possible by a series of innovations including: novel applications of a fine-tuned nanometer gap for passage of a single DNA or RNA mol.; thin layer microfluidics for sample loading and delivery; and programmable elec. fields for precise control of DNA or RNA movement. Detection methods include nanoelectrode-gated **tunneling current** measurements, dielec. **mol**. characterization, and atomic force microscopy/electrostatic force microscopy (AFM/EFM) probing for nanoscale reading of the nucleic acid **sequences**.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1997:655497 CAPLUS
DOCUMENT NUMBER: 127:313822
TITLE: Tunneling device and its production
INVENTOR(S): Gubin, Sergei Pavlovich; Kolesov, Vladimir Vladimirovich; Soldatov, Evgenii Sergeevich; Trifonov, Artem Sergeevich; Khanin, Vladimir Viktorovich; Khomutov, Genadii Borisovich; Yakovenko, Sergei Alexandrovich
PATENT ASSIGNEE(S): Samsung Electronics Co., Ltd, S. Korea
SOURCE: PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Russian
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9736333	A1	19971002	WO 1997-RU82	19970325
W: AL, AT, AU, BA, BB, BG, BR, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KP, KR, LC, LK, LR, LT, LU, LV, MG, MK, MN, MX, NO, NZ, PL, PT, RO, SE, SG, SI, SK, TR, TT, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
RU 2105386	C1	19980220	RU 1996-105544	19960326
RU 2106041	C1	19980227	RU 1996-112308	19960621
AU 9725792	A1	19971017	AU 1997-25792	19970325
EP 836232	A1	19980415	EP 1997-917492	19970325
EP 836232	B1	20030514		
R: DE, FR, GB, IT, NL				
CN 1189921	A	19980805	CN 1997-190420	19970325
CN 1097857	B	20030101		
JP 11500583	T2	19990112	JP 1997-534295	19970325
JP 3635409	B2	20050406		
PRIORITY APPLN. INFO.:			RU 1996-105544 A	19960326

RU 1996-112308 A 19960621
WO 1997-RU82 W 19970325

AB The tunneling device comprises input, output, and control electrodes separated by tunnel barriers; the tunnel barriers and inter-barrier spaces take the form of an ordered structure of **mols**. and clusters forming tunnel junctions, and each control electrode is disposed in the region of the **sequenced** structure of **mols**. and clusters. The dimensions and characteristics of these mols. and clusters ensure single-electron correlated tunneling of electrons in the device at relatively high (room) temps. The tunneling device is based on the principle of controllable correlated electron tunneling. The ability to control **tunnel current** opens up the possibility of constructing different electronic logic circuits based on single-electron **tunnel** junctions and creating single-electron analog and digital devices, in particular highly sensitive sensors. In manufacturing the tunneling device, input, output, and control electrodes are formed on a substrate, and an inert dielec. mol. matrix is then formed, incorporating ordered structures of active mols. and clusters, which act as localization centers for tunneling electrons and thus form single-electron tunnel junctions. The discrete **tunneling** effect of single **current** carriers through the **tunnel** barriers at room temperature achieved in this **tunneling** device can be used in a single-electron transistor and in the construction of single-electron logic circuits in which logical 1 and 0 are identified by the absence or presence of a single electron.

L3 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1995:559865 CAPLUS
DOCUMENT NUMBER: 122:286044
TITLE: Microscopic method for detecting micromotions
INVENTOR(S): Holzrichter, John F.; Siekhaus, Wigbert J.
PATENT ASSIGNEE(S): Regents of the University of California, USA
SOURCE: PCT Int. Appl., 26 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9506138	A1	19950302	WO 1994-US9678	19940825
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5620854	A	19970415	US 1995-402800	19950313

PRIORITY APPLN. INFO.: US 1993-111445 A 19930825

AB A scanning probe microscope, such as an atomic force microscope (AFM) or a scanning tunneling microscope (STM), is operated in a stationary mode on a site where an activity of interest occurs to measure and identify characteristic time-varying micromotions caused by biol., chemical, mech., elec., optical or phys. processes. The tip and cantilever assembly of an AFM is used as a micromech. detector of characteristic micromotions transmitted either directly by a site of interest or indirectly through the surrounding medium. Alternatively, the exponential dependence of the **tunneling current** on the size of the gap in the STM is used to detect micromech. movement. The stationary mode of operation can be used to observe dynamic biol. processes in real time and in a natural environment, such as polymerase processing of **DNA** for determining the **sequence** of a **DNA mol**.

L3 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1993:154883 CAPLUS
DOCUMENT NUMBER: 118:154883

TITLE: Electronic band structure of far-infrared gallium indium antimonide/indium arsenide (Ga1-xInxSb/InAs) superlattices
AUTHOR(S): Miles, R. H.; Schulman, J. N.; Chow, D. H.; McGill, T. C.
CORPORATE SOURCE: Hughes Res. Lab., Malibu, CA, 90265, USA
SOURCE: Semiconductor Science and Technology (1993), 8(1S), S102-S105
CODEN: SSTEET; ISSN: 0268-1242
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Results of tight-binding and eight-band k·p calcns. of the electronic band structure of long-wavelength Ga1-xInxSb/InAs superlattices are compared with existing exptl. energy-gap and absorption-coefficient data. The effective masses, band splittings, and absorption coeffs. observed in this system illustrate the potential of these structures for application in focal-plane-array systems demanding high detectivities or relaxed cooling requirements. Comparisons with Hg1-xCdxTe, the industry standard, are particularly favorable at longer wavelengths (8-12 μm and beyond), due to both a substantial reduction in **tunnel currents** and a suppression of impact-ionization-noise processes. The InSb- or Ga1-xInxAs-like nature of the interfaces should affect the energy gap of a Ga1-xInxSb/InAs superlattice; substantially larger optical absorption coeffs. are to be expected in structures with InSb-like interfaces. The present calcns. are in agreement with exptl. absorption spectra and with observed dependences of energy gaps on interfacial chemical, measured in samples in which the nature of the interfaces was controlled through apparatus-shuttering **sequences** and use of interrupts during growth by **mol**.-beam epitaxy.

L3 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1991:243895 CAPLUS
DOCUMENT NUMBER: 114:243895
TITLE: Scanning microscopes for chemical bond microscopy
INVENTOR(S): Rosser, Roy Jonathan; Williams, Brown
PATENT ASSIGNEE(S): UK
SOURCE: Brit. UK Pat. Appl., 9 pp.
CODEN: BAXXDU
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
GB 2235049	A1	19910220	GB 1989-14071	19890620

PRIORITY APPLN. INFO.: GB 1989-14071 19890620

AB A scanning microscope for detecting and differentiating mols. has a mol. or group of mols. attached to the probe tip. The probe interacts with the specimen via the attached mol. or mols. either by the **tunneling current**, as in a scanning **tunneling** microscope or by atomic forces as in an atomic force microscope. The mol. differences in either tunneling or atomic force with different mols. arise because of complementarity (or lack of it) of intermol. bonds. In one embodiment, **DNA sequences** are detected by probing with **DNA** monomers, looking for natural complementarity. Schematic views of the microscope are shown.

=> display l9 1-25 ibib abs

L9 ANSWER 1 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2006:137513 CAPLUS

TITLE: A general method for manipulating **DNA sequences** from any organism with **optical tweezers**
AUTHOR(S): Fuller, Derek N.; Gemmen, Gregory J.; Rickgauer, John Peter; Dupont, Aurelie; Millin, Rachel; Recouvreux, Pierre; Smith, Douglas E.
CORPORATE SOURCE: Department of Physics, University of California San Diego, 9500 Gilman Drive, La Jolla, CA, 92093-0379, USA
SOURCE: Nucleic Acids Research (2006), 34(2), e15
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mech. manipulation of single DNA mols. can provide novel information about DNA properties and protein-DNA interactions. Here we describe and characterize a useful method for manipulating desired **DNA sequences** from any organism with **optical tweezers**. Mols. are produced from either genomic or cloned DNA by PCR using labeled primers and are tethered between two optically trapped microspheres. We demonstrate that human, insect, plant, bacterial and viral sequences ranging from .apprx.10 to 40 kilobasepairs can be manipulated. Force-extension measurements show that these constructs exhibit uniform elastic properties in accord with the expected contour lengths for the targeted sequences. Detailed protocols for preparing and manipulating these mols. are presented, and tethering efficiency is characterized as a function of DNA concentration, ionic strength and pH. Attachment strength is characterized by measuring the unbinding time as a function of applied force. An alternative stronger attachment method using an amino-carboxyl linkage, which allows for reliable DNA overstretching, is also described.

L9 ANSWER 2 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1078071 CAPLUS
DOCUMENT NUMBER: 143:342218
TITLE: Methods and microfluidic apparatus for performing nucleic acid sequencing and detection using surface enhanced Raman spectroscopy
INVENTOR(S): Sundararajan, Narayanan; Sun, Lei; Zhang, Yuegang; Su, Xing; Chan, Selena; Koo, Tae-Woong; Berlin, Andrew A.
PATENT ASSIGNEE(S): Intel Corporation, USA
SOURCE: U.S. Pat. Appl. Publ., 24 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005221333	A1	20051006	US 2004-815264	20040331
PRIORITY APPLN. INFO.:			US 2004-815264	20040331

AB Methods and microfluidic apparatus for performing nucleic acid sequencing and detection using surface enhanced Raman spectroscopy are provided. Methods can be performed in a microfluidic channel to functionalize a solid support such as a bead with a single nucleic acid. The bead with a single nucleic acid attached may be transported and released upstream of a detector using **optical tweezers**. The **optical tweezers** are typically a gradient force **optical** trap that captures the single particle downstream from the laser beam. The released bead can then flow downstream and either become trapped in a restriction barrier or attached to a surface. Once the bead is confined, the **optical tweezers** can be removed so that they do not interfere with an **optical** detector downstream. Single

nucleotides can then be cleaved from the bead using an exonuclease. The single nucleotides may then be detected by surface enhanced Raman spectroscopy. The inclusion of a restriction barrier in a microfluidic channel and the immobilization of an optically transported bead allows removal of the **optical tweezers** from the **optical** path of a detection device, thereby preventing interference from the addnl. light source of the **optical tweezers** close to the collection volume of the detector.

L9 ANSWER 3 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1059908 CAPLUS
TITLE: A general method for manipulating **DNA sequences** from any organism with **optical tweezers**
AUTHOR(S): Fuller, Derek N.; Gemmen, Gregory J.; Rickgauer, John Peter; DuPont, Aurelie; Millin, Rachel; Recouvreux, Pierre; Schweitzer, Allen L.; Smith, Douglas E.
CORPORATE SOURCE: Dep. Phys., Univ. of California, San Diego, La Jolla, CA, 92093, USA
SOURCE: Proceedings of SPIE-The International Society for Optical Engineering (2005), 5930(Optical Trapping and Optical Micromanipulation II), 593013/1-593013/10
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Here we describe and characterize a method for manipulating desired **DNA sequences** from any organism with **optical tweezers**. Mols. are produced from either genomic or cloned DNA by PCR using labeled primers and are tethered between two optically trapped microspheres. We demonstrate that human, insect, plant, bacterial, and viral sequences ranging from .apprx.10 to 40 kbp can be manipulated. Force-extension measurements show that these constructs exhibit uniform elastic properties in accord with the expected contour lengths for the targeted sequences. Detailed protocols for preparing and manipulating these mols. are presented, and tethering efficiency is characterized as a function of DNA concentration, ionic strength, and pH. Attachment strength is characterized by measuring the unbinding time distribution as a function of applied force.
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:640255 CAPLUS
DOCUMENT NUMBER: 143:224343
TITLE: Dual binding modes for an HMG domain from human HMGB2 on DNA
AUTHOR(S): McCauley, Micah; Hardwidge, Philip R.; Maher, L. James, III; Williams, Mark C.
CORPORATE SOURCE: Department of Physics, Northeastern University, Boston, MA, 02115, USA
SOURCE: Biophysical Journal (2005), 89(1), 353-364
CODEN: BIOJAU; ISSN: 0006-3495
PUBLISHER: Biophysical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB High mobility group B (HMGB) proteins contain two HMG box domains known to bind without **sequence** specificity into the **DNA** minor groove, slightly intercalating between basepairs and producing a strong bend in the **DNA** backbone. We use **optical tweezers** to measure the forces required to stretch single DNA mols. Parameters describing DNA flexibility, including contour length and persistence length, are revealed. In the presence of nanomolar concns. of isolated HMG box A from HMGB2, DNA shows a decrease in its persistence

length, where the protein induces an average DNA bend angle of 114±21° for 50 mM Na+, and 87±9° for 100 mM Na+. The DNA contour length increases from 0.341±0.003 to 0.397±0.012 nm per basepair, independent of salt concentration In 50 mM Na+, the protein does not unbind even at high DNA extension, whereas in 100 mM Na+, the protein appears to unbind only below concns. of 2 mM. These observations support a flexible hinge model for noncooperative HMG binding at low protein concns. However, at higher protein concns., a cooperative filament mode is observed instead of the hinge binding. This mode may be uniquely characterized by this high-force **optical tweezers** experiment

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:621335 CAPLUS
DOCUMENT NUMBER: 143:224515
TITLE: Forced Unraveling of Nucleosomes Assembled on Heterogeneous DNA Using Core Histones, NAP-1, and ACF
AUTHOR(S): Gemmen, Gregory J.; Sim, Ronald; Haushalter, Karl A.; Ke, Pu Chun; Kadonaga, James T.; Smith, Douglas E.
CORPORATE SOURCE: Physics Department, University of California, San Diego, La Jolla, CA, 92093-0379, USA
SOURCE: Journal of Molecular Biology (2005), 351(1), 89-99
CODEN: JMOBAK; ISSN: 0022-2836
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Periodic arrays of nucleosomes were assembled on heterogeneous DNA using core histones, the histone chaperone NAP-1, and ATP-dependent chromatin assembly and remodeling factor (ACF). The mech. properties of these complexes were interrogated by stretching them with **optical tweezers**. Abrupt events releasing .apprx.55-95 base-pairs of DNA, attributable to the non-equilibrium unraveling of individual nucleosomes, were frequently observed This finding is comparable with a previous observation of 72-80 bp unraveling events for nucleosomes assembled by salt dialysis on a repeating sea urchin 5 S RNA positioning element, but the unraveling force varied over a wider range (.apprx.5-65 pN, with the majority of events at lower force). Because ACF assembles nucleosomes uniformly on heterogeneous **DNA sequences**, as in native chromatin, we attribute this variation to a dependence of the unraveling force on the **DNA sequence** within individual nucleosomes. The mean force increased from 24 pN to 31 pN as NaCl was decreased from 100 mM to 5 mM. Spontaneous DNA re-wrapping events were occasionally observed in real time during force relaxation. The observed wide variations in the dynamic force needed to unravel individual nucleosomes and the occurrences of sudden DNA re-wrapping events may have an important regulatory influence on DNA-directed nuclear processes, such as the binding of transcription factors and the movement of polymerase complexes on chromatin.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 6 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:570975 CAPLUS
DOCUMENT NUMBER: 143:92010
TITLE: Methods for high fidelity production of long nucleic acid molecules with error control
INVENTOR(S): Carr, Peter A.; Chow, Brian Y.; Jacobson, Joseph M.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 92 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2005059097	A2	20050630	WO 2004-US41478		20041210
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW					
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
US 2005255477	A1	20051117	US 2003-733847		20031210
PRIORITY APPLN. INFO.:			US 2003-733847	A	20031210
			US 2002-432556P	P	20021210

AB The invention relates to production of long nucleic acid **mols**. with precise user control over **sequence** content. Long error-free nucleic acid mols. can be generated in parallel from oligonucleotides immobilized on a surface, such as a microarray comprising redundantly overlapped oligonucleotides. The movement of the growing nucleic acid mol. can be controlled through the stepwise repositioning of the growing mol. Stepwise repositioning refers to the position of the growing mol. as it interacts with the oligonucleotides immobilized on the surface. Synthesis relies on annealing complementary pairs of oligonucleotides and extending them to produce longer oligonucleotide segments, until the full-length sequence is produced. This invention also relates to the prevention and/or removal of errors within nucleic acid mols. Mismatch recognition achieved through the use of mismatch binding proteins (e.g., MutS protein) can be used to control the errors generated during oligonucleotide synthesis, gene assembly, and the construction of nucleic acids. Mismatch protein-DNA complexes comprising error-containing DNA allows for separation and removal of errors, allowing selective amplification of error-free nucleic acids or correcting errors by nucleic acid repair.

L9 ANSWER 7 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:570974 CAPLUS
DOCUMENT NUMBER: 143:92009
TITLE: Methods for high fidelity production of long nucleic acid molecules with error control
INVENTOR(S): Carr, Peter A.; Chow, Brian Y.; Jacobson, Joseph M.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 91 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005059096	A2	20050630	WO 2004-US41268	20041210
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT,				

RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2005227235	A1	20051013	US 2003-733855	20031210
PRIORITY APPLN. INFO.:			US 2003-733855 A	20031210
			US 2002-432556P P	20021210

AB The invention relates to production of long nucleic acid **mols**. with precise user control over **sequence** content. Long error-free nucleic acid mols. can be generated in parallel from oligonucleotides immobilized on a surface, such as a microarray comprising redundantly overlapped oligonucleotides. The movement of the growing nucleic acid mol. can be controlled through the stepwise repositioning of the growing mol. Stepwise repositioning refers to the position of the growing mol. as it interacts with the oligonucleotides immobilized on the surface. Synthesis relies on annealing complementary pairs of oligonucleotides and extending them to produce longer oligonucleotide segments, until the full-length sequence is produced. This invention also relates to the prevention and/or removal of errors within nucleic acid mols. A preferred embodiment of the invention utilizes a force-feedback system using magnetic and/or **optical tweezers**, either sep. or in combination. The solid-phase support is magnetic in nature and held in a fixed equilibrium position by applying an elec field and magnetic field gradient created by the magnetic tweezers that opposes the electrophoretic force. As the oligonucleotides are annealed to the growing strand, the neg. charged phosphate backbone adds charge to the bead-strand complex, which moves the bead from its equilibrium position. Optically determined bead velocity and restoration force correspond to the number of bases added; therefore, the length of the added strand can be ensured to be correct.

L9 ANSWER 8 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER:	2005:472283 CAPLUS
DOCUMENT NUMBER:	143:20883
TITLE:	Methods for in vitro sorting of molecular and cellular libraries, such as a gene library, that are microencapsulated using water-in-oil-in-water emulsions
INVENTOR(S):	Tawfik, Dan; Bernath, Kalia; Aharoni, Amir; Peisajovich, Sergio; Griffiths, Andrew D.; Mastrobattista, Enrico; Magdassi, Shlomo
PATENT ASSIGNEE(S):	Yeda Research and Development Co., Ltd., Israel; Yissum Research Development Company of the Hebrew University of Jerusalem; Medical Research Council
SOURCE:	PCT Int. Appl., 124 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	1
PATENT INFORMATION:	

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005049787	A2	20050602	WO 2004-IL1079	20041124
WO 2005049787	C2	20050623		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:	US 2003-524045P	P	20031124

US 2004-618426P P 20041013

AB The present invention provides an in vitro system for compartmentalization of mol. or cellular libraries and provides methods for selection and isolation of desired mols. or cells from the libraries. The library includes a plurality of distinct mols. or cells encapsulated within a water-in-oil-in-water (w/o/w) emulsion. The emulation includes a continuous external aqueous phase and a discontinuous dispersion of water-in-oil droplets. The internal aqueous phase of a plurality of such droplets comprises a specific mol. or cell that is within the plurality of distinct mols. or cells of the library. According to a first aspect the present invention provides a gene library comprising a plurality of re-emulsified water-in-oil droplets, each droplet comprises an external water phase surrounding a central water-in-oil droplet, the internal water phase within each droplet comprises a genetic element, in vitro transcription-translation reaction system. To ensure that the genetic elements and gene products may not diffuse between primary water-in-oil droplets or between re-emulsified water-in-oil droplets, the-contents of each droplet must be isolated from the contents of the surrounding droplets, so that there is no or little exchange of gene products between the droplets over the timescale of the experiment The method of the present invention requires that there are only a limited number of genetic elements per droplet. This ensures that the gene product of an individual genetic element will be isolated from other genetic elements. Finally, the formation and the composition of the droplets must not interrupt with the function of the expression machinery of the genetic elements and the activity of the gene products. Preparation and sorting of w/o/w emulsions by FACS (fluorescence-activated cell sorting) were demonstrated using lacZ reporter selection from a pool of lacZ gene mutants. Compartmentalization and detection of PON1 (serum paraoxonase) gene variants in single Escherichia coli cells were also demonstrated.

L9 ANSWER 9 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:410306 CAPLUS
DOCUMENT NUMBER: 143:92784
TITLE: Single chromatin fiber stretching reveals physically distinct populations of disassembly events
AUTHOR(S): Pope, L. H.; Bennink, M. L.; van Leijenhorst-Groener, K. A.; Nikova, D.; Greve, J.; Marko, J. F.
CORPORATE SOURCE: Biophysical Techniques, Department of Science and Technology and MESA, University of Twente, Enschede, 7500 AE, Neth.
SOURCE: Biophysical Journal (2005), 88(5), 3572-3583
CODEN: BIOJAU; ISSN: 0006-3495
PUBLISHER: Biophysical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Eukaryotic DNA is packaged into the cell nucleus as a nucleoprotein complex, chromatin. Despite this condensed state, access to the **DNA sequence** must occur during gene expression and other essential genetic events. Here we employ **optical tweezers** stretching of reconstituted chromatin fibers to investigate the release of DNA from its protein-bound structure. Anal. of fiber length increase per unbinding event revealed discrete values of .apprx.30 and .apprx.60 nm. Furthermore, a loading rate anal. of the disruption forces revealed three individual energy barriers. The heights of these barriers were found to be .apprx.20 kBT, .apprx.25 kBT, and .apprx.28 kBT. For subsequent stretches of the fiber it was found that events corresponding to the .apprx.28 kBT energy barrier were significantly reduced. No correlation between energy barrier crossed and DNA length release was found. These studies clearly demonstrate that **optical tweezers** stretching of chromatin provides insight into the energetic penalties imposed by chromatin structure. Furthermore these studies reveal possible pathways via which chromatin may be disrupted during genetic code access.

REFERENCE COUNT: 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 10 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:185987 CAPLUS
TITLE: **Optical tweezers** measurements of DNA-protein interactions
AUTHOR(S): Gemmen, Gregory J.; Millin, Rachel; Sim, Ronald; Smith, Douglas E.
CORPORATE SOURCE: Dept. Physics, m/c 0379, UCSD, La Jolla, CA, 92093-0379, USA
SOURCE: Abstracts of Papers, 229th ACS National Meeting, San Diego, CA, United States, March 13-17, 2005 (2005), ANYL-170. American Chemical Society: Washington, D. C.
CODEN: 69GQMP
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB We present single mol. studies of histone-DNA interactions in chromatin complexes and of DNA looping enzymes. Mol. interactions are studied by manipulation and stretching of single DNA mols. with force-measuring **optical tweezers**. Nucleosome arrays are assembled in vitro using purified histones and chromatin assembly factors and detection of the unraveling of individual nucleosomes under force is presented. The distribution of unraveling forces and DNA lengths released are reported as a function of ionic conditions. **DNA** looping by **sequence** -specific **DNA** binding enzymes is also detected by stretching single **DNA mols**. within a microfluidic chamber to which protein solns. are introduced. This method allows tension dependent binding kinetics and binding forces to be measured. These studies provide new insights into protein-DNA interactions relevant in fundamental biochem. processes.

L9 ANSWER 11 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:185841 CAPLUS
TITLE: A general method for preparing **DNA sequences** for **optical tweezers** manipulation
AUTHOR(S): Smith, Douglas E.; Fuller, Derek; Dupont, Aurelie; Recouvreux, Pierre; Gemmen, Gregory J.; Millin, Rachel
CORPORATE SOURCE: Dept. Physics, m/c 0379, UCSD, La Jolla, CA, 92093-0379, USA
SOURCE: Abstracts of Papers, 229th ACS National Meeting, San Diego, CA, United States, March 13-17, 2005 (2005), ANYL-021. American Chemical Society: Washington, D. C.
CODEN: 69GQMP
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB Manipulation of single DNA mols. with nanometer-level position resolution and picoNewton-level force resolution is a powerful technique in the study of protein-DNA interactions. Here we present a general protocol for efficient preparation of **DNA sequences** from any organism for **optical tweezers** manipulation. We demonstrate this method in preparing genomic **DNA sequences** from Bacteriophage Lambda, E. Coli, Drosophila, Arabidopsis, and Human **DNA** samples. End labeled constructs up to 40 kilobasepairs are generated by PCR and single mols. are tethered to microspheres and manipulated using **optical tweezers**. We characterize DNA attachment kinetics, binding strength, tether length, and elastic properties. This sample preparation method is applicable to studies of a wide range of biochem. processes.

L9 ANSWER 12 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:442127 CAPLUS
DOCUMENT NUMBER: 139:193070
TITLE: Mechanical pulling through a nanopore can reveal the secondary structure of single RNA molecules
AUTHOR(S): Gerland, Ulrich; Bundschuh, Ralf; Hwa, Terence
CORPORATE SOURCE: Dept. of Physics, Center for Theoretical Biological Physics, Univ. of California at San Diego, La Jolla, CA, 92093-0319, USA
SOURCE: Los Alamos National Laboratory, Preprint Archive, Condensed Matter (2003) 1-9, arXiv:cond-mat/0306126, 5 Jun 2003
CODEN: LNCMFR
URL: http://xxx.lanl.gov/pdf/cond-mat/0306126
PUBLISHER: Los Alamos National Laboratory
DOCUMENT TYPE: Preprint
LANGUAGE: English

AB We investigate theor. the driven translocation of RNA mols. through narrow pores which allow single but not double strands to pass. In particular, we consider the situation where the driving force is exerted mech. with a device that records force-extension curves (FEC's), e.g. **optical tweezers**. We argue that such a setup can be used to determine the secondary structure, including pseudoknots, of RNA on a single-mol. level. For an exemplary **RNA sequence**, the Tetrahymena group I intron, we calculate such FEC's and demonstrate the reconstruction of the secondary structure explicitly. Our calcn. of the FEC's is based on the exptl. determined free energy rules for **RNA** secondary structures and a simplified model for the translocation kinetics, while the reconstruction uses only the FEC's and the **RNA** nucleotide **sequence**. We estimate that pulling speeds on the order of 1 am/s would be suitable for an exptl. implementation of the proposed method.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 13 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:879406 CAPLUS
DOCUMENT NUMBER: 138:165539
TITLE: Single molecule reactions of the enzyme LDH and of restriction endonucleases in the fluorescence microscope
AUTHOR(S): Nasanshargal, B.; Schafer, B.; Greulich, K. O.
CORPORATE SOURCE: Germany
SOURCE: Springer Series on Fluorescence (2002), 2(Fluorescence Spectroscopy, Imaging and Probes), 183-195
CODEN: SSFMCF; ISSN: 1617-1306
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. Two types of single mol. enzyme reactions can be directly observed in the fluorescence microscope: reactions, which convert nonfluorescing small substrate mols. into fluorescing products (or vice versa) and reactions of enzymes on macromols. stained by a fluorescence dye or visualized otherwise. As an example of the first type of reaction, the conversion of nonfluorescent NAD+ into fluorescing NADH, or vice versa, by a few mols. of lactate dehydrogenase in femtodroplets is described. The femtodroplet-pipetting method is essentially a subatomol technique with high accuracy. Lineweaver Burk plots are obtained with approx. the kinetic consts. of the enzyme known from conventional biochem. On the other hand, the femtodroplet-in-substrate method allows the observation of the action of individual enzyme mols. The second type of single **mol**. enzyme reactions is the **sequence**-specific cutting of individual **DNA mols**. held by **optical tweezers**. It is shown that such mols. can be characterized by the cutting (restriction) pattern generated by the restriction endonucleases ApaI, SmaI and EcoRI.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 14 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:226068 CAPLUS
DOCUMENT NUMBER: 136:306373
TITLE: Unzipping **DNA** with **optical** **tweezers**: high **sequence** sensitivity and force flips
AUTHOR(S): Bockelmann, U.; Thomen, Ph.; Essevaz-Roulet, B.; Viasnoff, V.; Heslot, F.
CORPORATE SOURCE: Laboratoire de Physique de la Matiere Condensee, Ecole Normale Superieure, Paris, 75005, Fr.
SOURCE: Biophysical Journal (2002), 82(3), 1537-1553
CODEN: BIOJAU; ISSN: 0006-3495
PUBLISHER: Biophysical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Force measurements are performed on single DNA mols. with an optical trapping interferometer that combines subpiconewton force resolution and millisecond time resolution A **mol**. construction is prepared for mech. unzipping several thousand-basepair **DNA** **sequences** in an in vitro configuration. The force signals corresponding to opening and closing the double helix at low velocity are studied exptl. and are compared to calcns. assuming thermal equilibrium We address the effect of the stiffness on the basepair sensitivity and consider fluctuations in the force signal. With respect to earlier work performed with soft microneedles, we obtain a very significant increase in basepair sensitivity: presently, sequence features appearing at a scale of 10 basepairs are observed When measured with the optical trap the unzipping force exhibits characteristic flips between different values at specific positions that are determined by the base sequence. This behavior is attributed to bistabilities in the position of the opening fork; the force flips directly reflect transitions between different states involved in the time-averaging of the mol. system.
REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 15 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:208974 CAPLUS
DOCUMENT NUMBER: 136:347370
TITLE: History of optical trapping and manipulation of small neutral particles, atoms, and molecules
AUTHOR(S): Ashkin, A.
CORPORATE SOURCE: Bell Laboratories Lucent Technologies, Holmdel, NJ, 07733, USA
SOURCE: Springer Series in Chemical Physics (2001), 67(Single Molecule Spectroscopy), 1-31
CODEN: SSCPDA; ISSN: 0172-6218
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review discusses the importance of **tweezers** and other **optical** methods in the study of single mols. in chemical, biol. and physics. Simple concepts such as momentum conservation, ray optics, and semiclassical rate equations are used to elucidate the forces and optical traps. In particular, the applications of tweezers to the study of single motor **mols**. as well as **DNA** folding and **sequencing** are described.
REFERENCE COUNT: 181 THERE ARE 181 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 16 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2002:31320 CAPLUS
DOCUMENT NUMBER: 136:80835
TITLE: Method and device for single **mol.** **sequencing** of nucleic acids using microparticles and fluorescence labeling
INVENTOR(S): Foeldes-Papp, Zeno; Holm, Johan
PATENT ASSIGNEE(S): Gnothis Holding SA, Switz.
SOURCE: PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002002225	A2	20020110	WO 2001-EP7460	20010629
WO 2002002225	A3	20030424		
WO 2002002225	C2	20030807		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
DE 10065626	A1	20020110	DE 2000-10065626	20001229
EP 1349649	A2	20031008	EP 2001-947427	20010629
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2005153284	A1	20050714	US 2002-311673	20010629
PRIORITY APPLN. INFO.:			DE 2000-10031840 A	20000630
			DE 2000-10065626 A	20001229
			WO 2001-EP7460 W	20010629

AB The invention concerns a method and device for sequencing single nucleic acids; all bases of at least one type in a nucleic acid are fluorescence-labeled; nucleic acids are immobilized onto microparticles; microparticles with immobilized sequences are transferred with laser tweezers into the sequencing unit; they are cleaved with exonucleases and products are transported by microchannel flow to fluorometric detection. 5'-Biotinylated nucleic acids are immobilized onto avidin or streptavidin coated particles.

L9 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:790919 CAPLUS
DOCUMENT NUMBER: 136:365885
TITLE: Taking light pressure serious: light as a quasimechanical microtool
AUTHOR(S): Greulich, Karl-Otto; Schaefer, Buerk; Monajembashi, Shamci
CORPORATE SOURCE: Inst. Mol. Biotech., Jena, D 07745, Germany
SOURCE: Proceedings of SPIE-The International Society for Optical Engineering (2001), 4430(Sixth Conference on Optics, 2000), 579-586
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. Light pressure may arise from absorption and can then be calculated as pressure equals intensity / vacuum velocity of light. Alternatively, it may result from scattering and is then called gradient force. In that

case a quality factor Q has to be introduced, which has to be determined by calibration. Its numerical value is between 0.05 and 0.3. By coupling a NdYAG laser into a microscope with a high numerical aperture objective scattering light pressure can be used to move micrometer-sized dielec. objects. Such **optical tweezers** can be calibrated and were used to measure forces needed to stretch individual DNA mols., and to measure forces exerted by the motor proteins myosin, kinesin and dynein non-calibrated **optical tweezers** are used to handle individual DNA mols. after their coupling to micrometer-sized microbeads. Using enzymes which cut **DNA mols.** in a **sequence** specific fingerprint-like pattern, it is possible to analyze **DNA** on a single **mol.** basis.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 18 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:474330 CAPLUS
DOCUMENT NUMBER: 135:208096
TITLE: Isolation of hyperthermophilic Archaea previously detected by sequencing rDNA directly from the environment
AUTHOR(S): Burggraf, Siegfried; Huber, Robert; Mayer, Thomas; Rossnagel, Petra; Rachel, Reinhard
CORPORATE SOURCE: Universitat Regensburg, Regensburg, 93053, Germany
SOURCE: Thermophiles (2001), 93-101. Editor(s): Reysenbach, Anna-Louise; Voytek, Mary; Mancinelli, Rocco. Kluwer Academic/Plenum Publishers: New York, N. Y.
CODEN: 69BKWQ
DOCUMENT TYPE: Conference
LANGUAGE: English

AB This paper describes the isolation of 3 microorganisms previously detected only by their 16 S rRNA sequences by a procedure that combines visual recognition of single cells in enrichment culture by phylogenetic staining and cloning by "**optical tweezers**.".

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 19 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:346757 CAPLUS
DOCUMENT NUMBER: 134:348963
TITLE: Protein-DNA fusion system for generation of new protein functions and screening combinatorial protein libraries in vitro
INVENTOR(S): Yanagawa, Hiroshi; Doi, Nobuhide
PATENT ASSIGNEE(S): Mitsubishi Chemical Corp., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 16 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
JP 2001128690	A2	20010515	JP 2000-244061		20000811
PRIORITY APPLN. INFO.:			JP 1999-239555	A	19990826
			JP 1999-239556	A	19990826

AB Protein-DNA fusion mols. and their use in generation and screening of new protein functions in vitro, are disclosed. A fusion protein of target protein and adapter protein is coupled to the encoding DNA via a ligand for the adapter protein. Biotin-binding protein, maltose-binding protein, poly-histidine peptide, glutathione-S-transferase, and antibodies, can be use as adapter protein. In vitro synthesis of protein-DNA fusion mols. in microcapsules and use of cDNA libraries is claimed. Use of beads as label

and cell sorter or **optical** pincette (**tweezers**, forceps) for screening, is also claimed. Use of phage surface displayed protein and ribosome for coupling are also claimed. The authors have developed a new method that permits the complete in vitro construction and selection of peptide or protein libraries. This method relies on an in vitro transcription/translation reaction compartmentalized in water in oil emulsions. In each emulsion compartment, streptavidin (STA)-fused polypeptides are synthesized and attached to the encoding DNA via its biotin label. The resulting protein-**DNA** fusion **mols**. recovered from the emulsion can be subjected to affinity selection based on the properties of the peptide portion, whose **sequence** can be determined from that of its **DNA**-tag. This method, named 'STABLE' (STA-biotin linkage in emulsions), should be useful for rapid in vitro evolution of proteins and for ligand-based selection of cDNA libraries.

L9 ANSWER 20 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2000:603970 CAPLUS
DOCUMENT NUMBER: 134:204644
TITLE: Molecular surgery of DNA based on electrostatic micromanipulation
AUTHOR(S): Yamamoto, Takatoki; Kurosawa, Osamu; Kabata, Hiroyuki; Shimamoto, Nobuo; Washizu, Masao
CORPORATE SOURCE: Department of Mechanical Engineering, Kyoto University, Kyoto, 606-8501, Japan
SOURCE: IEEE Transactions on Industry Applications (2000), 36(4), 1010-1017
CODEN: ITIACR; ISSN: 0093-9994
PUBLISHER: Institute of Electrical and Electronics Engineers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A novel method for the space-resolved dissection (mol. surgery) of DNA using electrostatic mol. manipulation is proposed and demonstrated. In conventional biochem., DNA-cutting enzymes and DNA are mixed in water, so the cutting reactions occur only by stochastic chances. In contrast, the present method is based upon a phys. manipulation and enables the reproducible cutting of DNA at any desired position along the DNA mol. In order to realize this space-resolved cutting, the target DNA is stretched straight by electrostatic orientation and anchored on a solid surface by dielectrophoresis, using the high-intensity (1 MV/m) high-frequency (1 MHz) field created in microfabricated electrodes. It is found that, for the enzymic cutting to occur, the DNA strand must be immobilized in such a way as to allow the enzyme to bind and interact with DNA. For this purpose, an electrode system is developed, in which DNA is anchored to the substrate only at the ends of the mol., leaving the middle free. The enzyme, on the other hand, is immobilized on a latex particle having 1-μm diameter, and **optical tweezers** are used to hold it and press it against the stretched and immobilized DNA. The enzymes used are: (1) DNaseI (cuts **DNA** regardless of the base **sequence**) and (2) HindIII (a restriction enzyme; cuts **DNA** at a specific **sequence**). It is demonstrated that, when a DNaseI-labeled bead is brought into contact with the immobilized DNA, DNA is cut instantaneously. On the other hand, when the restriction enzyme is used, the bead must be moved along the strand for a certain distance until it is finally cut. Our interpretation for this enzyme dependence is that the restriction enzyme has to get into the grooves of DNA to find the restriction sites, so the condition for the mol. contour fitting of the DNA and the enzyme are stricter compared with the case of the simple backbone-cutting enzyme DNaseI. The technique presented in this paper is expected to realize space-resolved mol. surgical operations, not just limited to dissections, but also for chemical modifications, or even insertion of genes.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 21 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:346911 CAPLUS
DOCUMENT NUMBER: 133:262022
TITLE: Single molecule DNA restriction analysis in the light microscope
AUTHOR(S): Schafer, Burk; Gemeinhardt, Helgard; Uhl, Volker; Greulich, Karl Otto
CORPORATE SOURCE: Institut fur Molekulare Biotechnologie, Jena, D-07708, Germany
SOURCE: Single Molecules (2000), 1(1), 33-40
CODEN: SGMCF7; ISSN: 1438-5163
PUBLISHER: Wiley-VCH Verlag Berlin GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A combination of single mol. fluorescence intensity anal. and optical mapping is developed to identify individual fluorescently labeled DNA mols. on the basis of restriction patterns generated by different enzymes. Fluorescently labeled lambda-phage DNA mols. each bound to a polystyrene microsphere as a handle are held and moved by **optical tweezers**. The single DNA mols. are stretched in a hydrodynamic flow. The restriction endonucleases ApaI, SmaI and EcoRI with one, three and five expected cutting sites on the lambda-phage DNA mol. are used for enzymic digestion of the DNA mols. The DNA restrictions are observed after microinjection of the enzyme into the flow towards the DNA mol. in real time (video frequency) on a microscope cover slide. The fluorescence intensity of the DNA fragments is measured and their length in terms of base pairs is calculated Comparison with the length expected from **sequence** data reveals a single **DNA** fragment sensitivity and an accuracy of +/-16%.
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 22 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1999:728905 CAPLUS
DOCUMENT NUMBER: 132:61482
TITLE: The active digestion of uniparental chloroplast DNA in a single zygote of Chlamydomonas reinhardtii is revealed by using the **optical tweezer**
AUTHOR(S): Nishimura, Yoshiki; Misumi, Osami; Matsunaga, Sachihiro; Higashiyama, Tetsuya; Yokota, Akiho; Kuroiwa, Tsuneyoshi
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo, 113-0033, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1999), 96(22), 12577-12582
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The non-Mendelian inheritance of organelle genes is a phenomenon common to almost all eukaryotes, and in the isogamous alga Chlamydomonas reinhardtii, chloroplast (cp) genes are transmitted from the mating type pos. (mt+) parent. In this study, the preferential disappearance of the fluorescent cp nucleoids of the mating type neg. (mt-) parent was observed in living young zygotes. To study the change in cpDNA **mols**. during the preferential disappearance, the cpDNA of mt+ or mt- origin was labeled sep. with bacterial aadA gene **sequences**. Then, a single zygote with or without cp nucleoids was isolated under direct observation by using **optical tweezers** and investigated by nested PCR anal. of the aadA sequences. This demonstrated that cpDNA mols. are digested completely during the preferential disappearance of mt- cp nucleoids within 10 min, whereas mt+ cpDNA and mitochondrial DNA are protected from the digestion. These results indicate that the

non-Mendelian transmission pattern of organelle genes is determined immediately after zygote formation.
REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 23 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1999:284593 CAPLUS
DOCUMENT NUMBER: 131:140853
TITLE: Aspects of DNA assembly: extension, lithography and recognition
AUTHOR(S): Shivashankar, G. V.; Libchaber, A.
CORPORATE SOURCE: Centre for Studies for Physics and Biology, The Rockefeller University, New York, NY, 10021, USA
SOURCE: Current Science (1999), 76(6), 813-818
CODEN: CUSCAM; ISSN: 0011-3891
PUBLISHER: Current Science Association
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 32 refs. In this paper we describe the micromanipulation of single genomic **DNA** and the lithog. representation of its **sequence** information on a biochip. An **optical tweezer** combined with force detection using light backscattering and a force cantilever is used to manipulate single mols. Using this we probe the flexibility of a DNA template and its use as a mech. detector to study DNA-protein interactions. We then use this approach to directly monitor the extension of a single DNA polymer beyond its contour length, due to its unwinding, induced by the polymerization of RecA protein. Finally the application of a localized light source for bio-mol. lithog. is presented. We describe micropatterning DNA mols. on a solid substrate for specific bio-mol. recognition. The ability to manipulate, fabricate addressable DNA arrays and specifically recognize genomic DNA mols. opens the possibility of studying the mechanisms underlying genetic processes and biol. networks.
REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 24 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 1998:23658 CAPLUS
DOCUMENT NUMBER: 128:188903
TITLE: Direct measurement of DNA molecular length in solution using **optical tweezers**: detection of looping due to binding protein interactions
AUTHOR(S): Sakata-Sogawa, K.; Kurachi, Masashi; Sogawa, Kazuhiro; Fujii-Kuriyama, Yoshiaki; Tashiro, Hideo
CORPORATE SOURCE: Photodynamics Research Center, Laboratory for Photo-Biology, The Institute of Physical and Chemical Research (RIKEN), 19-1399 Koeji, Nagamachi, Aoba-ku, Sendai, 980, Japan
SOURCE: European Biophysics Journal (1998), 27(1), 55-61
CODEN: EBJOE8; ISSN: 0175-7571
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB DNA looping is caused by the interaction between DNA binding proteins located at sep. positions on a DNA mol. and may play an important role in transcription regulation. A system to stretch single DNA mols. and to measure changes in mol. length has been developed. DNA mols. were prepared and 5' end-labeled by PCR amplification. Two beads and the intervening DNA mol. were trapped and manipulated independently with dual trap **optical tweezers**. The trapped DNA mol. was then stretched and the extension (the distance between the two beads) was measured. The extension at the specific tension force of 30 pN was calculated and used as a mol. length. The mol. length was found to be proportional

to the base pair number The rise per residue was calculated to be 3.31±0.05 A. The length measurement was applied to **DNA** fragments containing GC box **sequences** at two different locations separated by a distance of 2.428 kbp. The addition of GC box binding transcription factor Sp1 shortened the mol. length, suggesting DNA looping forms as a result of interaction between transcription factors.

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 25 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1997:113444 CAPLUS
DOCUMENT NUMBER: 126:115424
TITLE: Optical trap for detection and quantitations of subzeptomolar quantities of analytes
INVENTOR(S): Weetall, Howard Hayyam; Helmerson, Kristian Peter; Kishore, Roni Bakhru
PATENT ASSIGNEE(S): National Institute of Standards and Technology, USA; Weetall, Howard Hayyam; Helmerson, Kristian Peter; Kishore, Roni, Bakhru
SOURCE: PCT Int. Appl., 23 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9641154	A1	19961219	WO 1996-US10007	19960607
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA				
US 5620857	A	19970415	US 1995-473979	19950607
CA 2223576	AA	19961219	CA 1996-2223576	19960607
CA 2223576	C	20011030		
AU 9662719	A1	19961230	AU 1996-62719	19960607
EP 871861	A1	19981021	EP 1996-921508	19960607
R: AT, BE, CH, DE, ES, FR, GB, IT, LI, NL				
JP 11507437	T2	19990629	JP 1996-502148	19960607

PRIORITY APPLN. INFO.: US 1995-473979 A 19950607
WO 1996-US10007 W 19960607

AB Tightly focused beams of laser light are used as "**optical tweezers**" to trap and manipulate polarizable objects such as microspheres of glass or latex with diams. on the order of 4.5 μm. When analytes are allowed to adhere to the microspheres, small quantities of these analytes can be manipulated, thus allowing their detection and quantitations of the analytes are extremely small. Illustrative examples include measuring the strength needed to break antibody-antigen bonds and the detection of **DNA sequences**.